

Developing a maintenance framework for the NZSCC

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Image: New Zealand Seafloor Classification (75 groups) - from Stephenson et al., 2022

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Executive summary

The New Zealand Seafloor Community Classification (NZSCC) is a national-scale numerical community classification which depicts compositional turnover of 1,716 taxa (demersal fish, reef fish, benthic invertebrates and macroalgae) classified into 75 groups representing seafloor communities. The Department of Conservation has actively committed to maintaining, improving, and promoting the use of the NZSCC, which will subsequently facilitate the use of the classification as an input for marine spatial planning and reporting at both national and regional scales.

A key component of a maintenance framework for the NZSCC is being able to assess the ability of the classification to represent (discriminate between) different seafloor communities. This assessment is important because understanding the performance of the classification in describing biodiversity patterns is a key step in determining how the classification should be interpreted, and if the classification should be updated. In this report, we describe an approach for validating the NZSCC which considers the classification strength (i.e., identify whether the NZSCC represents different seafloor communities), evaluates the underlying statistical model, and considers heterogeneity in environmental coverage and statistical uncertainty of the NZSCC. The validation approach, which is provided as reproducible R code, was exemplified using relatively large independent evaluation datasets for two of the four biotic groups used in the NZSCC (demersal fish and benthic invertebrates).

There was a reasonable coverage of the 75 NZSCC groups by the evaluation data (n = 41 and n = 21 NZSCC groups for demersal fish and benthic invertebrates, respectively). The Global-R classification strength values were 0.53 and 0.46 (and significant at the 1% level) for demersal fish and benthic invertebrates, respectively, indicating that the NZSCC groups define biologically distinctive environments as assessed by the independent evaluation data. The proportion of significant inter-group differences were very high (95% and 97% for demersal fish and benthic invertebrates, respectively) suggesting NZSCC groups were distinct from each other in their taxonomic composition. The relationship between the evaluation datasets and the underlying statistical model were also moderate to high, and there no obvious effects of these relationships being affected by environmental coverage (i.e., the geographical and environmental spread of the samples used to develop the NZSCC) or the statistical uncertainty of the NZSCC.

Additionally, the evaluation datasets contained robust estimates of taxa abundances which provided an opportunity to test whether the NZSCC, which was developed using presence / absence data, reflects patterns in taxa abundances (i.e., abundance-weighted seafloor communities). Model validation metrics using abundance evaluation data were encouraging (albeit lower than for presence/absence) suggesting that the NZSCC, can at least in part, broadly represent variation in abundance-weighted communities.

Results of the validation exercise are used to develop a maintenance framework that includes the following elements:

- The description of a process for validating the NZSCC;
- The description of a process to determine when to trigger running of an updated or new model;
- Decision tree framework to determine when to release an updated or new classification.

1 Introduction

The New Zealand Seafloor Community Classification (NZSCC, Figure 1) is a national-scale numerical community classification commissioned by the Department of Conservation (DOC) which depicts compositional turnover of 1,716 taxa (demersal fish, reef fish, benthic invertebrates and macroalgae) classified in 75 groups representing seafloor communities (Petersen et al., 2021; Stephenson et al., 2021a; Stephenson et al., 2022). The NZSCC relies on both biotic and physical/environmental data to represent the interconnection between biological assemblages and the environment. The NZSCC is a significant advance on previous numerical classifications, such as the Marine Environmental Classification (MEC) and Benthic Optimised MEC (BOMEC) (Snelder et al., 2007; Leathwick et al., 2012), in terms of taxonomic and environmental data coverage (Stephenson et al., 2022). The NZSCC allows identification of environments that are likely to host rare or unusual communities as well as identifying geographic areas (which may consist of multiple New Zealand SCC groups) that are most representative of New Zealand seafloor communities as a whole, for example, in a Marine Protected Area (MPA) network planning process. However, to ensure the continual use of the NZSCC by central government, local and regional councils, universities and other interested parties, a robust maintenance framework must be set in place. By building a reliable maintenance framework, DOC actively commits to maintaining, improving and promoting the use of the NZSCC, which will subsequently facilitate the use of the classification as an input for marine spatial planning and reporting at both national and regional scales.



Figure 1. The New Zealand Seafloor Community Classification (75 groups) from Stephenson et al., 2021; 2022. Colours broadly correspond to similarities/differences in predicted compositional turnover (i.e., similar colours represent similar communities).

A key component of a maintenance framework for the NZSCC is being able to assess the ability of the classification to represent (discriminate between) different seafloor communities. This assessment is important because understanding the performance of the classification in describing biodiversity patterns is required for judging when and how the classification should be used in management decisions (i.e., the confidence to place in the classification) but is also a key step in determining if the classification should be updated. Should the NZSCC poorly represent different seafloor communities (or the classification could be improved) then it will be important to consider how and when the NZSCC could be updated.

In this study, potential improvements to the NZSCC are explored and results are used to develop a maintenance framework for the NZSCC. Stephenson et al. (2022) assessed the NZSCC's ability to discriminate across classification levels using the biological data included in the classification in an analysis of similarities test (ANOSIM), (i.e., using internal data validation) (Clarke and Warwick, 2001). This assessment showed that the 75-group classification explained the most variation with the fewest number of groups based on data used to develop the models. However, validation of statistical models should ideally be undertaken with independent validation data (Friedman et al., 2001). In this report the NZSCC was validated using independent evaluation data for demersal fish and benthic invertebrates (i.e., data which was not used to develop the classification). Additionally, the availability of abundance estimates for these evaluation datasets provides the added opportunity to test whether the NZSCC - which was developed using presence / absence data - can reflect abundance-weighted seafloor communities. Should the NZSCC reflect patterns in communities accounting for abundance this would provide additional utility for managers since understanding of spatial patterns in species' abundances facilitates the identification of the most important areas for marine protection. For example, key ecosystem functions and services such as filter feeding, biomass production, and reef formation are density-dependent (Lohrer et al., 2004; Spaak et al., 2017; Rowden et al., 2020). Results of this analysis are then used to develop a maintenance framework that includes the following elements:

- The description of a process for validating the NZSCC;
- The description of a process to determine when to trigger running of an updated model or a new model;
- Decision tree framework to determine when to release an updated or new classification.

Recommendations and guidance are summarised and provided in grey boxes at the end of each section.

2 The description of a process for validating the NZSCC

2.1 Technical background: developing the NZSCC

To facilitate the interpretation of the validation methods and the maintenance framework, the methods used to generate the NZSCC are briefly summarised.

The underpinning statistical model for the NZSCC is a community-based (multivariate) modelling method called Gradient Forests (GF, Ellis et al., 2012; Pitcher et al., 2012). GF uses species distribution data to control the selection, weighting, and transformation of (spatially

explicit) environmental predictors to maximise their correlation with species compositional turnover and establish where along the range of environmental gradients important compositional changes occur (Ellis et al., 2012). These transformed environmental layers (representing species compositional turnover) can then be (hierarchically) classified to discrete spatial groups that capture variation in species composition and turnover (Stephenson et al., 2021a; Stephenson et al., 2022). The NZSCC was tuned using biotic data from demersal fish, reef fish, benthic invertebrates and macroalgae. The final classification (75 groups, NZSCC) aims to represent seafloor communities across these four biotic groups (Petersen et al., 2021).

In addition to the spatial estimates of compositional turnover and subsequent estimates of seafloor community groups (the classification), two spatially explicit uncertainty estimates were generated: standard deviation of the predicted taxa compositional turnover and environmental coverage. The environmental coverage provides an indication of the parts of the environmental space that, for example, contain many samples – meaning more confidence can be placed on the relationships and the predictions for compositional turnover and SSC groupings in such areas (and conversely, less confidence placed in SCC groupings in areas within environmental space that have less samples). The uncertainty estimates of community compositional turnover provide an important indication of the variability in the (GF) modelling estimates. Together, these uncertainty estimates provide complementary measures of uncertainty to be considered by managers (Stephenson et al., 2021b). For a more detailed description of the methods and outputs of the NZSCC, see Stephenson et al. (2021a); Stephenson et al. (2022).

2.2 Methods for validating the NZSCC

To validate the NZSCC, independent evaluation data was collated for two of the four biotic groups used to generate the NZSCC: demersal fish and benthic invertebrates.

Demersal fish biomass data were extracted from MPI database *trawl* (for dates 01/01/2017 – 01/01/2022, MPI rep log 14760). Only samples using bottom trawls, undertaken within the New Zealand Territorial Sea (TS) and Exclusive Economic Zone (EEZ) – hereafter referred to as the New Zealand marine environment – were retained for analysis. Demersal fish biomass (kg) was converted to presence / absence for the first part of the validation analysis. As a second step to assess whether the NZSCC could also represent variation in abundance-weighted community data, demersal fish biomass was standardised by trawl swept area (in km⁻², the product of fishing gear door width and the distance fished for each trawl). The final demersal fish evaluation dataset contained presence/ absence and standardised biomass for 268 species from 4099 bottom trawls (Figure 2, A).

Benthic invertebrate densities (number of individuals per 1000 m²) from seafloor imagery data collected using NIWA's Deep Towed Imaging System (DTIS) were collated from multiple surveys (Bowden et al., 2019; Anderson et al., 2020; Anderson et al., 2023 and references therein). Only samples contained within the New Zealand marine environment were retained. No further data grooming of this dataset was necessary because these data were collated, groomed and the taxonomy standardised as part of DOC project POP2021-02 (Anderson et al., 2023). The final benthic invertebrate evaluation dataset contained presence/ absence and standardised densities for 74 taxa from 735 DTIS transects (Figure 2, B).

For simplicity, the standardised demersal fish biomass and benthic invertebrate densities are both referred to as *abundance* from this point forward.



Figure 2. Location of independent evaluation data for demersal fish (A) and benthic invertebrates (B) overlaid on the environmental coverage. Environmental coverage depicts the predicted confidence that can be placed in the predictions of compositional turnover underpinning the NZSCC based on the number and location of the biotic records used to train the model. Values range from low (i.e., no samples in the dataset with those environmental conditions: low confidence in predictions) to high (i.e., many samples with those environmental conditions: high confidence in predictions) within the New Zealand marine environment.

Validation of the NZSCC using demersal fish and benthic invertebrate presence/absence data was undertaken using two different approaches.

First, the classification strength of the 75-group NZSCC was assessed. This assessment was undertaken separately for demersal fish and benthic invertebrates following the approach described in Stephenson et al. (2022) based on methods developed by Bowden et al. (2011). Briefly, classification strength was assessed using an analysis of similarities test (ANOSIM) (Clarke and Warwick, 2001) of the multivariate presence/absence taxonomic data tagged with NZSCC groups based on spatial location. The classification strength is measured as the Global-R statistic, which was calculated as the difference in ranked biological similarities arising from all pairs of replicate sites between different groups, and the average of all rank similarities within groups, adjusted by the total number of sites. Global-R is equal to 1 if all replicates within groups are more like each other than any replicates from different groups and is approximately 0 if there is no group structure. Significance levels of the ANOSIM statistics were tested with a randomisation procedure based on the null hypothesis of no group structure. All ANOSIM analyses were undertaken in R v4.0.3 (R Core Team, 2020)

using the *Vegan* (v 2.6) package (Oksanen et al., 2013). Only groups with >5 unique occurrences were included in the analysis as per Stephenson et al. (2022).

Second, the relationship between community composition (using presence/absence data) and predicted compositional turnover (outputs from the GF model) was explored. This assessment was undertaken separately for demersal fish and benthic invertebrates following modified methods described in Stephenson et al. (2018). Briefly, extended biological dissimilarities (shortest dissimilarity = 0.8) using the Bray–Curtis dissimilarity measure with the functions vegdist and stepacross implemented in the Vegan package were calculated for each sample location of the demersal fish and benthic invertebrate evaluation datasets. The use of extended biological distances improves ordinations with high beta diversity, i.e., when there are many sites with no species in common (De'ath, 1999). Correlations (Mantel test, implemented in the Vegan package) were then calculated between these biological dissimilarities and the equivalent distances in the predicted compositional turnover (Euclidean distance calculated using the multivariate estimate of transformed environmental variable layers – termed environmental distance here). Relationships between biological dissimilarities and the paired environmental distances were visualized in scatter plots; given the size of the dissimilarity matrices, a random subset of 50,000 points were selected for these plots (approximately 7% for demersal fish and 20% for benthic invertebrates). To explore whether the relationship between the community composition and predicted compositional turnover was affected by the statistical uncertainty from the GF modelling (underpinning the NZSCC), each point in the figure was coloured according to the environmental coverage, and separately, the standard deviation of the predicted species compositional turnover.

Finally, to explore whether the NZSCC represents variation in abundance-weighted communities, both validation approaches were repeated but using the abundance estimates of demersal fish and benthic invertebrates.

2.3 Results

2.3.1 Broad description of the evaluation data

Demersal fish

Demersal fish evaluation data (4099 bottom trawls) occurred across a broad range of water depths (Figure 3) and NZSCC groups (*n* = 49), of which, 41 groups had more than 5 samples (the minimum required for the ANOSIM analysis). These groups were: 9, 12, 13, 16, 17, 18, 20, 21, 22, 23, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 39, 40, 45, 47, 50, 51, 52, 53, 54, 55, 56, 57, 63, 64, 65, 67, 68, 69, 70, 73 and 75. See Petersen et al. (2021) for descriptions of these groups.





Bottom trawls occurred primarily in parts of the environmental space that would be considered well represented in the NZSCC (n = 3718 in environmental coverage > 0.5). That is, in areas with high environmental coverages which would indicate a higher confidence in spatial predictions from the GF models. However, some bottom trawls (n = 360) and fewer still (n = 21) occurred in moderate (0.1 - 0.5) and low (< 0.1) areas of environmental coverage, respectively (see Section 3 for details on the importance of having evaluation data in areas of moderate – low environmental coverage).

Benthic invertebrates

Benthic invertebrate evaluation data (735 DTIS transects) occurred across a broader range of water depths than demersal fish (Figure 4) but due to the lower number of samples, these occurred across a narrower range of NZSCC groups (n = 32 for benthic invertebrates) and even fewer groups had more than 5 samples (n = 22). The groups with sufficient data to assess classification strength using benthic invertebrate evaluation data were: 4, 5, 6, 8, 9, 10, 11, 12, 13, 14, 16, 17, 18, 20, 21, 22, 28, 30, 36, 37, 47 and 64. See Petersen et al. (2020) for descriptions of these groups.





DTIS transects were more evenly spread across the environmental coverage than the demersal fish (n = 507 in areas with high environmental coverage; n = 117 in areas with moderate environmental coverage; and n = 111 areas with low environmental coverage).

2.3.2 Evaluating the NZSCC

There were sufficient data to evaluate the discriminatory power of 55% and 29% of the NZSCC groups using demersal fish and benthic invertebrate evaluation data, respectively (Table 1). Given the large extent of the New Zealand marine environment, it is unlikely that evaluation data would cover all NZSCC groups (with sufficient replication) without a targeted sampling programme. To put this into context, the large dataset used to *develop* the NZSCC (630,997 records across the four biotic groups occurring at 39,766 unique locations) only covered 76% of NZSCC groups for the demersal fish and 91% of NZSCC groups for the benthic invertebrates (Stephenson et al., 2022).

The Global-R values were 0.53 and 0.46 (and significant at the 1% level) for demersal fish and benthic invertebrates (respectively), indicating that the NZSCC groups define biologically distinctive environments as assessed by completely independent evaluation data (Table 1). For context, the Global-R values for the NZSCC as assessed by internal training data used in the GF models was higher for demersal fish (R value: 0.72, Stephenson et al., 2022) but lower for benthic invertebrates (R value: 0.25, Stephenson et al., 2022), noting that internal training datasets usually result in higher performance metrics compared to independent evaluation data (Friedman et al., 2001).

The Global-R values presented here are particularly encouraging because evaluations of previously developed numeric seafloor classifications for the New Zealand marine environment – the MEC (Snelder et al., 2007) and BOMEC (Leathwick et al., 2012) – using independent evaluation data suggested that neither of these classifications were able to

provide adequate spatial distribution or discrimination of benthic habitats and faunal assemblage composition using DTIS transect samples (Bowden et al., 2011). Using independent evaluation data, Bowden et al. (2011) found that the MEC and BOMEC classifications had mean Global-R values less than 0.06.

Of the NZSCC groups with sufficient independent evaluation data, the proportion of significant inter-group differences were very high (95% and 97% for demersal fish and benthic invertebrates, respectively - Table 1) suggesting NZSCC groups were distinct from each other in their taxonomic composition. Pairwise differences are further explored in the Supplementary Materials. The supplementary materials show the pairwise differences between the 75 groups of the NZSCC for demersal fish and benthic invertebrates using presence/absence and abundance data (which should be read by column – that is, it is not a mirrored correlation matrix). Groups codes (columns and rows) are colour coded to match the colours used in Figure 1, and broadly represent similarities/differences in predicted compositional turnover - similar colours represent similar communities. Where data are available and there are significant differences in species composition, these are indicated by ***, whereas where data are available and there are no significant differences in species composition, these are indicated by orange cells with *ns* (for not significant). Where there were no data available to test differences between groups, cells are left blank. Of particular importance when interpreting these pairwise plots is identifying groups which are not significantly different from other groups that are expected to be very different in their species composition. For example, Group 36 was not significantly different to a wide variety of other groups using the demersal fish presence/absence data, noting that Group 36 shares similar environmental conditions to most groups (i.e., it occurs in the middle of the transformed environmental space) and in contrast discriminates well when using the benthic invertebrate presence/absence dataset. See Section 3 for further considerations when exploring pairwise differences between NZSCC groups.

Biotic group	Proportion of NZSCC groups > 5 unique occurrences	Proportion of significant inter-group differences	Global-R value
Demersal fish	0.55	0.95	0.53
Benthic invertebrates	0.29	0.97	0.46

Table 1. Results of the pair-wise analysis of similarities test (ANOSIM) analysis of the NZSCC using presence/absence evaluation data for demersal fish and benthic invertebrates.

There was a strong and moderate positive relationship between community compositions and predicted compositional turnover for demersal fish (Mantel r = 0.66) and benthic invertebrates (Mantel r = 0.32), respectively (Figure 5, A and C). In other words, as community composition increased in dissimilarity (extended Bray-Curtis dissimilarity) so too did the environmental distance (i.e., the dissimilarity in the predicted community compositions). There were no obvious patterns (clustering) in environmental coverage values for either demersal fish or benthic invertebrates (Figure 5, A and C). If the relationship between community compositions and predicted compositional turnover was expected to be affected by the uncertainty associated with low sampling in certain environments (i.e., low environmental coverage), then we would expect to see red / orange points distributed on the edges of the data point cloud. Similarly, there was no pattern in the distribution of the standard deviation of mean compositional turnover across the benthic invertebrate community composition and predicted compositional turnover (Figure 5, D). However, there appeared to be a slight pattern of increasing standard deviation of mean compositional turnover for samples with increasing demersal fish compositional dissimilarity and increasing environmental distance (Figure 5, C). That is, there was greater variability in the prediction of environmental distance at higher values, noting that this variability was very low compared to the mean prediction (i.e., maximum standard deviation of the mean was 0.004 compared to a predicted inter-group distance of more than 0.4) (Figure 5, C).



Figure 5. Extended Bray-Curtis dissimilarity against distance in transformed environmental space (Euclidean distance) of randomly sampled presence / absence samples (n = 50,000) for demersal fish (A and B) and benthic invertebrates (C and D). Colours represent measures of uncertainty: environmental coverage (A and C) and standard deviation of mean compositional turnover (B and D).

2.3.3 Evaluating whether the NZSCC can represent abundance-weighted communities

To explore whether the NZSCC represents variation in abundance-weighted communities, both validation approaches were repeated using the standardised abundance estimates of demersal fish and benthic invertebrates. Similar to the evaluation using presence/absence data, there was:

- A higher proportion of significant inter-group differences (97% for both demersal fish and benthic invertebrates,
- Table 2) and see Supplementary Materials
- All the Global-R values were significant at the 1% level (ANOSIM)
- The Global-R values were 0.53 and 0.38 for demersal fish and benthic invertebrates (respectively) (which is slightly lower for the benthic invertebrates when using abundance compared to presence / absence data) indicating that the NZSCC groups define biologically distinctive environments even when using abundance data (
- Table 2).

This finding is meaningful as the analysis provides evidence that the NZSCC can, at least in part, reflect patterns of benthic taxa' abundances, which is an important consideration for marine protection.

There was a positive relationship between demersal fish and benthic invertebrate abundance-weighted community compositions and predicted compositional turnover (Mantel r = 0.59 and 0.23 respectively, Figure 6, A and C). This relationship was not as strong as when using presence/absence data, particularly for the benthic invertebrate abundanceweighted data where a much more variable relationship was observed (Figure 6Figure 6, C).

Given the abundance-weighted data and the presence / absence data occur in the same locations, the same patterns of uncertainty were observed when using the weightedabundance estimates as those already described in section 2.3.2 (Figure 6, A, B, C and D).

Table 2. Results of the pair-wise analysis of similarities test (ANOSIM) analysis of the NZSCC using standardised abundance evaluation data for demersal fish and benthic invertebrates.

Biotic group	Proportion of groups > 5 unique occurrences	Proportion of significant inter-group differences	Global-R value
Demersal fish	0.55	0.97	0.53
Benthic invertebrates	0.29	0.97	0.38



Figure 6. Extended biological distances (extended Bray-Curtis dissimilarity) against distance in transformed environmental space (Euclidean distance) of random abundance samples (n = 10,000) for demersal fish (A & B) and benthic invertebrates (C & D). Colours represent measures of uncertainty: environmental coverage (A & C) and standard deviation of mean compositional turnover (B &D).

2.4 Caveats to interpretation

The analysis presented here represents an independent evaluation data for two of the four biotic groups used in the NZSCC using a (relatively) modest sample number. Ideally, data would be available for each biotic group across all NZSCC groups where they are expected to occur (i.e., macroalgae do not occur below the photic zone and therefore will not be present in all NZSCC groups). The approach provided here is transferable to other biotic groups and larger dataset (i.e., the analysis can be repeated with macroalgal and reef fish datasets without modifications in the approach). However, the results presented in Section 2 should not be interpreted as "final" and model performance may be lower for other biotic groups, or areas not sampled with the available dataset. In particular, model performance may be lower in areas of low environmental coverage (for which there was low sample numbers here, Figure 2), i.e., NZSCC groups for which there was little training data underpinning the GF models.

2.5 Summary and guidance

Summary:

- Two methods for evaluating the NZSCC were outlined, one of which considers heterogeneity in environmental coverage and statistical uncertainty of the NZSCC.
- The approach was exemplified using independent evaluation data for two of the four biotic groups used in the NZSCC (demersal fish and benthic invertebrates). This approach is transferable to other biotic groups (i.e., the analysis can be repeated with macroalgal and reef fish datasets without modifications in the approach).
- Repeatable R code is provided in the supplementary materials allowing routine re-assessment of NZSCC model fits as and when needed (see Section 3).

Guidance:

- It is recommended that independent presence/absence data from all four biotic groups (demersal fish, reef fish, benthic invertebrates and macroalgae) is used to fully evaluate the NZSCC.
- The same evaluation approach can be used to explore whether seafloor communities represented in the NZSCC also account for abundance.
- Descriptive statistics of the data provide a means for identifying data availability and coverage.
- Evaluation of the NZSCC should consider heterogeneity in environmental coverage and statistical uncertainty.

3 The process to determine when to trigger an updated or new model

Periodic collation of biological data and updating of spatially explicit environmental variables (e.g., every 5- 10 years) allows the evaluation, and if necessary, updating or generation of a new NZSCC. In this section guidance is developed for assessing when to update or run a new GF model (i.e., how to determine when there is sufficient new environmental and biological data available to trigger updating/running a new statistical model). Should the NZSCC be updated, or a new GF model and classification be developed, the performance of these new outputs should be assessed and compared to the existing GF model and NZSCC and only carried forward if the new outputs outperform current predictions (see Section 0).

3.1 Updating the NZSCC using previously collated data *and* newly collated biotic data

The exact number of additional (newly collated) biotic samples that would provide improved predictive power to the NZSCC is unknown. However, when the NZSCC has poor evaluation scores using new samples (i.e., repeating the process outlined in Section 2), or if new samples provide additional information for rare species (i.e., when the addition of samples results in new taxa included in the GF models) or occur in previously low or unsampled parts of the New Zealand marine environment (i.e., locations with low (< 0.1) – moderate (0.1 – 0.5) environmental coverage), it will be important to further explore whether these additional samples would affect estimates of compositional turnover. In the first instance, undertaking an evaluation of the NZSCC using the new data is suggested (i.e., by using the process outlined in Section 2), and in particular, exploring the pairwise differences between groups. Should groups with high uncertainty in compositional turnover and / or low environmental coverage (all information provided in Petersen et al., 2021) show no significant differences with other groups, this may indicate a need to test the inclusion of these data in an updated NZSCC.

To assess whether new samples provide additional information on species richness, exploring an indicator of richness is recommended. For example, ES50 (Hulbert index), which is the statistically expected number of unique species in a random sample of 50 occurrence records within each biotic group (e.g., Costello et al., 2017; Chaudhary and John Costello, 2023). Specifically, examining ES50 for each biotic group stratified by bioregion (Stephenson et al., 2023). Such an assessment provides a means for stratifying the samples based on large regions that represent broad-scale biodiversity patterns that are relatively homogeneous (stable over space and time) with distinct environmental conditions and biological contents, and are biologically relevant (Costello et al., 2017). Where ES50 increases with the addition of newly collated data, re-running an NZSCC model may be appropriate.

At the scale of the New Zealand marine environment, the quality of environmental data using in the NZSCC varies spatially, i.e., some layers may be most robust, particularly close to shore. For example, the sediment classification layer (Sed.class) is more robust inshore due to higher sampling underpinning the spatial data layers (Bostock et al., 2019). Despite the large influence that substrate is expected to have on demersal and benthic species composition (Ruiz et al., 2009), this environmental predictor variable had relatively low

influence on seafloor community compositional turnover, most likely due to incomplete substrate distributions (e.g., incomplete information on the distribution of hard substrata such as rocky reefs).

The accuracy of spatial predictions from species' distribution models (including GF) rely on robust and accurate spatially explicit environmental variables (e.g., see implications of inaccurate spatially explicity variables on model performance in Anderson et al., 2016). However, the uncertainty or inaccuracy of spatially explicit environmental variables are rarely explored or accounted for (Bowden et al., 2021). The spatially explicit environmental variables used in the GF models were updated / compiled as part of the development of the NZSCC. These environmental variables therefore represent the best available estimates at present, but they still contain inaccuracies that may be remedied in subsequent updates. The influence that these new environmental layers may have on the spatial predictions of the NZSCC are unknown, however, as a preliminary assessment, updated environmental variables can be compared to previously used environmental variables. If, for example, there are substantial differences between any of the 'old' and 'new' environmental layers (for example, > 10% difference across 5% of the study area) and these occur in areas where compositional turnover is predicted to be high, then this could trigger the updating of the NZSCC (i.e., see an example using bathymetry data in Figure 7). Noting, that some parts of the environmental space are currently poorly sampled (e.g., areas with water depths > 2500m) and therefore may underestimate compositional turnover (see section 4 for considerations and decisions on when to re-run GF models).

Although different environmental predictors have more or less influence in the GF model (and therefore on the resulting predictions and the NZSCC), prioritising the updating of environmental predictors based on these influences is not recommended since they may change in subsequent NZSCC updated models. That said, the development and integration of robust and complete estimates of substrate type could be prioritised both because it is known to have limitations in its current form (i.e., less accuracy further from coast) and such a layer could be used within the NZSCC but separately from the modelling process (e.g., as a group 'modifier'). Group modifiers are qualitative descriptions used to separate out specific areas within a group, i.e., where the classification does not provide the necessary level of description for the data (United States. National Ocean Service and United States. Federal Geographic Data Committee, 2012). For example, a deep-water group could be split into ridges vs plains vs trenches (features which are known to occur within the same group), but which may have very different biota (Rowden et al., 2017).



Figure 7. Mean (\pm SD) relative compositional turnover along the range of water depth (bootstrapped combined GF models of samples from all biotic groups (R2) used in the NZSCC), adapted from Figure S6 of Stephenson et al., 2022. Coloured boxes broadly (subjectively) indicate parts of the depth gradient where very high (red), high (orange) and low (blue) compositional turnover are predicted to occur. E.g., should updated bathymetry layers suggest there are large differences (> 10% difference with previous bathymetry layer) where high compositional turnover is expected (approx. 0 – 50m), this could trigger the development of a 'new' a GF model with the updated bathymetry layer.

3.2 Developing a 'new' NZSCC to address limitations of the current NZSCC

There are several known limitations of the NZSCC (i.e., see the "Improving the classification" section in Stephenson et al., 2022). Broadly, these are:

- Temporal mismatch between the biological and environmental data: The long temporal span over which biotic samples were collected (primarily 1900 – 2016) means that there is a mismatch between the temporal collection window of biological data and that of the environmental variables which were mostly compiled from data collected since 2000. The NZSCC would benefit from having only biological data sampled over the same time as the long-term mean environmental data (from 2000 onwards) since it is assumed that the relationship between samples and environmental predictors is likely to be more relevant / realistic if the biological and environmental timescales are matched.
- 2. The omission of abundance (density/biomass) data in the NZSCC: Abundance estimates were available for reef and demersal fish, but previously not for benthic invertebrates nor the macroalgae data (in sufficient quantity and geographical coverage); therefore, only presence/absence data was used in the NZSCC. It was not known whether the seafloor communities represented by the NZSCC also represented abundance/density/biomass of seafloor taxa. However, further analysis from this study has indicated that seafloor demersal fish and benthic invertebrate communities represented by the NZSCC may also be broadly representative of

biomass and density of demersal fish and benthic invertebrates, respectively. But whether a similar relationship exists for reef fish and macroalgae is unknown.

New collations of biological data may provide avenues for evaluating, and if necessary, developing a 'new' NZSCC which could address limitations 1 and 2. Specifically for the temporal mismatch between environmental and biological data (limitation 1), any data collected after 2004 for reef fish, 2016 for demersal fish, 2015 for benthic invertebrates and 2018 for macroalgae will provide relevant data to attempt generating a 'new' model with matching biotic and environmental temporal scales. The number of biotic samples and geographic coverage of these groups will be important considerations for deciding whether to run a new GF model (or not). There are no definitive rules with regards to appropriate sample number or geographic coverage. However, using the large dataset available for the NZSCC, estimates of compositional turnover were found to be stable across bootstrap models (i.e., using 5000 samples for demersal fish and benthic invertebrates, 3320 for macroalgae and 339 for reef fish Stephenson et al., 2022). Therefore, this could be used as a rule of thumb for the sample number that has appropriate spatial / environmental coverage, noting that biotic groups with the lowest sample number – macroalgae and reef fish – also had the lowest internal model fits. These low model fits imply that the existing NZSCC may particularly benefit from a greater number of samples for macroalgae and reef fish (see section 3.1). As a starting point, it would be reasonable to generate a 'new' model when there are approximately 5000 samples for demersal fish and benthic invertebrates, 3000 samples for macroalgae and 300 samples for reef fish from the year 2000 onwards. These samples can include both existing and newly collated samples, but only those after 2000. However, to evaluate the performance of the new model, we recommend retaining 10% of completely independent data (more or less evenly spread across geographic space) to independently evaluate the 'new' model and 'existing' model (the NZSCC). It may be that a new model with a smaller temporal window does not perform as well as the existing NZSCC simply because a 'new' model may have fewer taxa to inform the estimates of compositional turnover than the existing NZSCC.

To address the omission of abundance data (limitation 2), the same approach as described for limitation 1 can be used. That is, when there is sufficient abundance data available (5000 samples for demersal fish and benthic invertebrates, 3000 samples for macroalgae and 300 samples for reef fish), a 'new' model can be generated and evaluated. Noting that the 'existing' model's ability to discriminate abundance-weighted seafloor communities using independent (withheld) evaluation data performed better than expected and therefore the NZSCC may still provide adequate interim predictions until a 'new' model using abundance data is developed.

The development of updated or 'new' GF models as suggested in a number of cases described above can be undertaken in a time efficient manner: in the first instance, new models can be generated without undertaking a bootstrap approach (greatly reducing the modelling complexity and time taken to produce outputs for evaluation). In addition, the development of an approach for evaluating and comparing the new models with the existing NZSCC (Section 2) provides a systematic and cost-efficient approach that can be routinely undertaken by those with moderate data analysis and R coding skills. It is recommended that biotic and environmental data are collated / updated periodically at the same time (e.g., a reasonable time based on the rate of new data availability could be every 5 - 10 years). These updated data are a valuable resource that will have a wide array of

uses. For example, building on biological and environmental data collated and updated for the development of the NZSCC, over 600 taxa' distribution models were generated that are freely available online and have been used within a number of national and regional government projects: <u>https://doc-marine-data-deptconservation.hub.arcgis.com/</u>, Stephenson & Brough et al. (2023).

The past 30 years have seen a growing sophistication in the types of statistical models applied in ecology, with impetus from substantial advances in both statistics and computing. For example, the use of gradient forests to provide quantitative descriptions of large-scale biodiversity patterns, as applied here, represented a significant improvement in model accuracy compared to earlier classification methods such as regression trees. Future statistical developments have the potential to provide substantially better approaches for dealing with some of the limitations described above. Where statistical advances provide a more accurate and more nuanced understanding of the available data and improve model accuracy they should be assessed to determine if their adoption would improve the performance of the NZSCC.

Summary:

Future iterations of the NZSCC could be based on:

1) Updating the NZSCC using previously collated data *and* newly collated biotic and/or environmental data.

And/or

2) Developing a 'new' NZSCC which would specifically try to address some of the limitations of the existing NZSCC by using different biotic and environmental datasets or statistical approaches.

Guidance:

- Whether updating or developing a 'new' GF models, periodically collating /updating biotic and environmental data is required (e.g., a reasonable time based on the rate of new data availability could be every 5 – 10 years).
- In the first instance, these new data should be used to assess whether the existing NZSCC is performing well / the data provides any important additional coverage before any new modelling is undertaken (e.g., using R code and approaches outlined in Section 2).
- The updating or development of a 'new' GF models should be generated without undertaking a bootstrap approach (greatly reducing the modelling complexity and time taken to produce outputs for evaluation).
- Performance of 'new' or updated NZSCC models should be evaluated for their predictive ability (by retaining approx. 10% of completely independent data, more or less evenly spread out across the geographic space) and only carried forward if these perform better than the existing NZSCC model (see section 4 for further details).
- 1) Updating the NZSCC
- The exact number of additional (newly collated) biotic samples that would provide improved predictive power to the NZSCC is unknown. However, assessing the likelihood of improving the model is recommended by:
 - Assessing the predictive power of the existing NZSCC using new samples (i.e., as outlined in Section 2).
 - Assessing if new samples provide additional information for rare species (e.g., using the ES50 indicator).
- Environmental variables used in the NZSCC represent the best available estimates but will undoubtedly have improved accuracy in future updates.
 - As a preliminary assessment of whether updated environmental variables would influence the predictions of compositional turnover, exploring the magnitude of difference between 'old' and 'new' environmental variables is recommended.
 - E.g., if there are substantial differences (> 10% difference in places) and these occur in areas where compositional turnover is predicted to be high or very high, then this could trigger the updating of the model.
- See Section 4 for how newly collated biotic and environmental data can be considered together when deciding to update the GF model.

Summary (continued):

- 2) Developing a 'new' NZSCC
- Collation of new presence/absence and abundance data can provide ways of addressing limitations of the NZSCC with regards to the temporal mismatch between the biological and environmental data and lack of abundance estimates in the seafloor communities of the NZSCC.
- As a rule of thumb, it is recommended that the development of a 'new' model could be undertaken when approximately 5000 samples for demersal fish and benthic invertebrates, 3000 samples for macroalgae and 300 samples for reef fish are available. These new data could either be abundance data or presence / absence data from the year 2000 onwards.
- Assessing improvement of a 'new' NZSCC is recommended following the same approached outlined for updating the NZSCC.

4 Decision tree framework to determine when to release an updated or new classification.

This section provides guidance on when to release an updated or 'new' classification following running a new statistical model versus maintaining the status quo (e.g., statistical comparisons between iterations of the NZSCC). The most pressing reason for updating the NZSCC would be poor predictive performance of the existing NZSCC. The current NZSCC has high predictive power as assessed by a reasonable set of independent evaluation data for demersal fish and benthic invertebrates (noting that this is a subset of biotic groups used in the NZSCC). This finding is an encouraging result, but periodic and systematic re-assessment using a full suite of biotic and updated environmental data, and if necessary, updating will ensure that NZSCC remains the best available information for describing the seafloor communities of the New Zealand environment (e.g., see Section 3).

Following collation of presence/absence (and if available, abundance) data for all biotic groups (Figure 8), evaluating the NZSCC using the approach outlined in Section 2 is recommended (Figure 8, box 3). Should the existing NZSCC perform poorly when evaluated using the newly collated data (Figure 8, box 3 and 4, particularly concentrating on pairwise comparison between groups and samples in areas with low / moderate environmental coverage) the GF model (without bootstrapping) should be updated using previous, and newly collated, data (Figure 8, box 6). Should there be sufficient data to generate a GF model where biological and environmental data have matching temporal scales (i.e., > 5000 samples for demersal fish and benthic invertebrates, 3000 samples for macroalgae and 300 samples for reef fish from the year 2000 onwards, Figure 8, box 5 a 'new' GF model should be generated (Figure 8, box 6). The performance of any updated/new GF models should be undertaken with withheld evaluation data (completely independent dataset which is at least 10% of available data) and the performance of the updated/new GF model and classification compared to the existing NZSCC using the process described in Section 2. Should the updated/new model outperform and provide tangible differences in spatial distributions, then generating final outputs from the updated/new NZSCC should be undertaken (i.e., bootstrapping) (Figure 8, box 7). When considering abundance data for the development of a 'new' NZSCC, the approach is similar: should there be sufficient data to generate a GF model using abundance data for all biotic groups (i.e., > 5000 samples for demersal fish and benthic invertebrates, 3000 samples for macroalgae and 300 samples for reef fish) (Figure 8, box 3) then a new GF model and classification can be generated (with no bootstrapping) and compared to the existing NZSCC using withheld evaluation data (Figure 8, box 6). Should this new GF model and classification perform better than the existing NZSCC, then a fully bootstrapped approach can be undertaken (Figure 8, box 7).



Figure 8. Decision tree for updating or developing a 'new' NZSCC following periodic collation of biotic data. Note, box 6 represents both updated/'new' GF models and box 7 represents both an updated or 'new' NZSCC.

Following an update of environmental variables (Figure 9), an initial assessment between the existing and the newly updated environmental variables is recommended (Figure 9, box 2). Should there be differences between existing and the newly updated environmental variables (e.g., > 10% in environmental values across 5% of the study area), then exploration of where these differences occur relative to the environmental gradient, and the rate of compositional turnover within the GF models should be undertaken (Figure 9, box 3). Should differences between old and new environmental variables occur in locations where there is high compositional turnover, then generating a new GF model and classification is recommended (Figure 9, box 6). Equally, if the differences between old and new environmental variables occur in previously unsampled areas (Figure 9, box 4) and newly collated biological data now provides samples in these parts of the environmental gradient (Figure 9, box 5), then generating a new GF model and classification using the updated environmental variables and the newly collated biotic data is recommended (Figure 9, box 6). Should this new GF model and classification perform better than the NZSCC, then a fully bootstrapped approach can be undertaken (Figure 9, box 7).



Figure 9. updating or developing a 'new' NZSCC following periodic collation of environmental data. Note, box 6 represents an updated GF model and box 7 represents an updated NZSCC.

5 Summary of recommendations and guidance for a maintenance framework for the NZSCC

Summary

• Guidance was provided on when to release an update or make a new classification following running a new statistical model versus maintaining the status quo.

Guidance

• Decision trees presented in Section 4 for assessing the NZSCC, following periodic collation of biotic and/or environmental data, provide a cost-effective framework for ongoing maintenance and updates or developments to the NZSCC.

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